

DMCI0099.ST25.txt  
SEQUENCE LISTING

<110> Havkin-Frenkel, Daphna  
Podstolski, Andrzej  
Dixon, Richard A.

<120> Vanillin Biosynthetic Pathway Enzyme From Vanilla Planifolia

<130> DMCI0099

<150> 09/462,576  
<151> 2000-05-22

<150> PCT/US98/14895  
<151> 1998-07-15

<150> 60/052,604  
<151> 1997-07-15

<150> 60/272,415  
<151> 2001-02-28

<160> 25

<170> PatentIn version 3.1

<210> 1  
<211> 1071  
<212> DNA  
<213> Vanilla planifolia

<400> 1  
atggcagcta agctcctctt ctctactc ttcctggtct ccgccctctc cgtcgcgctc 60  
gccggtttcg aagaagacaa tccaatccgg tccgttacac aaaggcctga ctcgattgag 120  
cctgccatcc tcggcgctct tggcagttgc cgccacgcct tccacttcgc acggttcgcc 180  
cgcaggtacg ggaagagcta cggatcggag gaggagatca agaagagggt cgggatcttc 240  
gtggagaatc tagcgtttat ccggtccact aatcggaagg atctgtcgta taccctagga 300  
atcaaccaat tcgccgacct gacctgggag gaattccgga ccaatcgctt tgggtgcggcg 360  
cagaactgct cggcgactgc gcatggaaac caccggtttg tcgatggcgt gcttcctgta 420  
acgagggatt ggagggagca agggatagtg agccctgtaa aggaccaagg aagctgtgga 480  
tcttgtgga ctttcagtac tactggagca ctagaggctg catatacaca gctaactgga 540  
aagagcacat cattatctga acagcaactt gtggactgtg cctcagcatt caataacttt 600  
ggatgcaatg gaggtttgcc ttcccaagcc tttgaatacg ttaagtacaa tggaggcatc 660  
gacacagaac agacttatcc ataccttgggt gtcaatggta tctgcaactt caagcaggag 720  
aatgttggtg tcaaggtcat tgattcgata aacatcacc cgggtgctga ggatgagttg 780  
aagcatgcag tgggcttgggt gcgtccagtt agcgttgcatt ttgaggttgt gaaaggtttc 840  
aatctgtaca agaaagggtg atacagcagt gacacctgtg gaagagatcc aatggatgtg 900  
aaccacgcag ttcttgccgt cggttatgga gtcgaggacg ggattcctta ttggctcatc 960

## DMCI0099.ST25.txt

aagaactcat ggggtacaaa ttgggggtgac aatgggtact ttaagatgga actcggcaag 1020

aacatgtgtg gtgttgcaac ttgcgcattc tatccattg tggctgtgta g 1071

&lt;210&gt; 2

&lt;211&gt; 352

&lt;212&gt; PRT

&lt;213&gt; Vanilla planifolia

&lt;400&gt; 2

Met Ala Ala Lys Leu Leu Phe Phe Leu Leu Phe Leu Val Ser Ala Leu  
1 5 10 15Ser Val Ala Leu Ala Gly Phe Glu Glu Asp Asn Pro Ile Arg Ser Val  
20 25 30Thr Gln Arg Pro Asp Ser Ile Glu Pro Ala Ile Leu Gly Val Leu Gly  
35 40 45Ser Cys Arg His Ala Phe His Phe Ala Arg Phe Ala Arg Arg Tyr Gly  
50 55 60Lys Ser Tyr Gly Ser Glu Glu Glu Ile Lys Lys Arg Phe Gly Ile Phe  
65 70 75 80Val Glu Asn Leu Ala Phe Ile Arg Ser Thr Asn Arg Lys Asp Leu Ser  
85 90 95Tyr Thr Leu Gly Ile Asn Gln Phe Ala Asp Leu Thr Trp Glu Glu Phe  
100 105 110Arg Thr Asn Arg Leu Gly Ala Ala Gln Asn Cys Ser Ala Thr Ala His  
115 120 125Gly Asn His Arg Phe Val Asp Gly Val Leu Pro Val Thr Arg Asp Trp  
130 135 140Arg Glu Gln Gly Ile Val Ser Pro Val Lys Asp Gln Gly Ser Cys Gly  
145 150 155 160Ser Trp Thr Phe Ser Thr Thr Gly Ala Leu Glu Ala Ala Tyr Thr Gln  
165 170 175Leu Thr Gly Ser Thr Leu Ser Glu Gln Gln Leu Val Asp Cys Ala Ser  
180 185 190Ala Phe Asn Asn Phe Gly Cys Gly Gly Leu Pro Ser Gln Ala Phe Glu  
195 200 205

DMCI0099.ST25.txt

Tyr Val Lys Tyr Asn Gly Gly Ile Asp Thr Glu Gln Thr Tyr Pro Tyr  
210 215 220

Leu Gly Val Met Gly Ile Cys Asn Phe Lys Gln Glu Asn Val Gly Val  
225 230 235 240

Lys Val Ile Asp Ser Ile Asn Ile Thr Leu Gly Ala Glu Asp Glu Leu  
245 250 255

Lys His Ala Val Gly Leu Val Arg Pro Val Ser Val Ala Phe Glu Val  
260 265 270

Val Lys Gly Phe Asn Leu Tyr Lys Lys Gly Val Tyr Ser Ser Asp Thr  
275 280 285

Cys Gly Arg Asp Pro Met Asp Val Asn His Ala Val Leu Ala Val Gly  
290 295 300

Tyr Gly Val Glu Asp Gly Ile Pro Tyr Trp Leu Ile Lys Asn Ser Trp  
305 310 315 320

Gly Thr Asn Trp Gly Asp Asn Gly Tyr Phe Lys Met Glu Leu Gly Lys  
325 330 335

Asn Met Cys Gly Val Ala Thr Cys Ala Ser Tyr Pro Ile Val Ala Val  
340 345 350

<210> 3<211> 7<212> PRT<213> Artificial Sequence<220><223> Novel Sequence

<400> 3

Gly Val Leu Pro Val Thr Arg  
1 5

<210> 4

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 4

Asn Ser Trp Gly Thr Asn Trp Gly Asp Asn Gly Tyr Phe  
1 5 10

<210> 5

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 5

Gly Phe Asn Leu Tyr Lys  
1 5

<210> 6

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 6

Gln Gly Ile Val Ser Pro Val Lys  
1 5

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 1a 5

<220>

<221> misc\_feature

<222> (3)..(3)

<223> N= Inosine

<220>

<221> misc\_feature

<222> (6)..(6)

<223> N= Inosine

<220>

<221> misc\_feature

<222> (9)..(9)

<223> N= Inosine

<220>

<221> misc\_feature

<222> (12)..(12)

<223> N= Inosine

<220>

<221> misc\_feature

<222> (15)..(15)

<223> N= I

<220>

<221> misc\_feature

<222> (18)..(18)

<223> N= I

<400> 7

ggngtnc tnc cngtnacncg

1008774-022802

<210> 8  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Primer 1a 5

<220>  
 <221> misc\_feature  
 <222> (3)..(3)  
 <223> N= Inosine

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> N= Inosine

<220>  
 <221> misc\_feature  
 <222> (9)..(9)  
 <223> N= Inosine

<220>  
 <221> misc\_feature  
 <222> (12)..(12)  
 <223> N= Inosine

<220>  
 <221> misc\_feature  
 <222> (15)..(15)  
 <223> N= Inosine

<220>  
 <221> misc\_feature  
 <222> (18)..(18)  
 <223> N= Inosine

<400> 8  
 cgngtnacng gnagnacncc

20

<210> 9  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Primer 2a 5

<220>  
 <221> misc\_feature  
 <222> (3)..(3)  
 <223> N= t or c

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> N= Inosine

<220>

<221> misc\_feature  
 <222> (12)..(12)  
 <223> N= Inosine

<220>  
 <221> misc\_feature  
 <222> (15)..(15)  
 <223> N= Inosine

<220>  
 <221> misc\_feature  
 <222> (18)..(18)  
 <223> N= t or c

<220>  
 <221> misc\_feature  
 <222> (24)..(24)  
 <223> N= Inosine

<220>  
 <221> misc\_feature  
 <222> (27)..(27)  
 <223> N= t or c

<220>  
 <221> misc\_feature  
 <222> (30)..(30)  
 <223> N= t or c

<220>  
 <221> misc\_feature  
 <222> (33)..(33)  
 <223> N= Inosine

<220>  
 <221> misc\_feature  
 <222> (36)..(36)  
 <223> N= t or c

<220>  
 <221> misc\_feature  
 <222> (39)..(39)  
 <223> N= t or c

<400> 9  
 aantcntggg gnacnaantg gggnganaan ggntanttna a

41

<210> 10  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Primer 2b 5

<220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> N= c or t

<220>  
 <221> misc\_feature

10087714.022800T

<222> (4)..(4)  
 <223> N= g or a

<220>  
 <221> misc\_feature  
 <222> (7)..(7)  
 <223> N= g or a

<220>  
 <221> misc\_feature  
 <222> (10)..(10)  
 <223> N= Inosine

<220>  
 <221> misc\_feature  
 <222> (13)..(13)  
 <223> N= g or a

<220>  
 <221> misc\_feature  
 <222> (16)..(16)  
 <223> N= g or a

<220>  
 <221> misc\_feature  
 <222> (19)..(19)  
 <223> N= Inosine

<220>  
 <221> misc\_feature  
 <222> (25)..(25)  
 <223> N= g or a

<220>  
 <221> misc\_feature  
 <222> (28)..(28)  
 <223> N= Inosine

<220>  
 <221> misc\_feature  
 <222> (31)..(31)  
 <223> N= Inosine

<220>  
 <221> misc\_feature  
 <222> (37)..(37)  
 <223> N= Inosine

<220>  
 <221> misc\_feature  
 <222> (40)..(40)  
 <223> N= g or a

<400> 10  
 nttnaantan ccnttntcnc cccanttngt nccccangan tt

42

<210> 11  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Primer 3a 5

<220>

<221> misc\_feature

<222> (3)..(3)

<223> N= Inosine

<220>

<221> misc\_feature

<222> (6)..(6)

<223> N= t or c

<220>

<221> misc\_feature

<222> (9)..(9)

<223> N= t or c

<220>

<221> misc\_feature

<222> (12)..(12)

<223> N= Inosine

<220>

<221> misc\_feature

<222> (15)..(15)

<223> N= t or c

<400> 11

ggnttnaanc tntanaa

17

<210> 12

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 3b5

<220>

<221> misc\_feature

<222> (1)..(1)

<223> N= c or t

<220>

<221> misc\_feature

<222> (4)..(4)

<223> N= g or a

<220>

<221> misc\_feature

<222> (7)..(7)

<223> N= Inosine

<220>

<221> misc\_feature

<222> (10)..(10)

<223> N= g or a

<220>

<221> misc\_feature

<222> (13)..(13)

<223> N= g or a

10087714.022802  
208220-4T/800T



<220>  
 <221> misc\_feature  
 <222> (16)..(16)  
 <223> N= Inosine

<400> 12  
 nttntanagn ttnaancc

18

<210> 13  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> 4HBS P1a

<400> 13  
 ggaattccat atggcagcta agtcctctt c

31

10087714-022802  
 208220"4T/2802  
 <210> 14  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> 4HBS P1b

<400> 14  
 cgcggatccc tacacagcca caatggg

27

<210> 15  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> 4HBS P2a

<400> 15  
 cccatagtct tcctgtaacg agggattgg

29

<210> 16  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> 4HBS P3b

<400> 16  
 cccctcgaga tggcagctaa gctcctcttc

30

<210> 17  
 <211> 28

<212> DNA  
<213> Artificial Sequence

<220>

<223> 4HBS P3b

<400> 17  
ccccactagt ctacacagcc acaatggg

28

<210> 18  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Oligo 1

<400> 18  
gtatctgagc tcaaaaatgg cagctaagct cctc

34

<210> 19  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Oligo 2

<400> 19  
catagaggat ccctacacag ccacaatggg ataa

34

<210> 20  
<211> 360  
<212> PRT  
<213> Arabidopsis thaliana

<400> 20

Met Ser Ala Lys Thr Ile Leu Ser Ser Val Val Leu Val Val Leu Val  
1 5 10 15

Ala Ala Ser Ala Ala Ala Asn Ile Gly Phe Asp Glu Ser Asn Pro Ile  
20 25 30

Arg Met Val Ser Asp Gly Leu Arg Glu Val Glu Glu Ser Val Ser Gln  
35 40 45

Ile Leu Gly Gln Ser Arg His Val Leu Ser Phe Ala Arg Phe Thr His  
50 55 60

Arg Tyr Gly Lys Lys Tyr Gln Asn Val Glu Glu Met Lys Leu Arg Phe  
65 70 75 80

## DMCI0099.ST25.txt

Ser Ile Phe Lys Glu Asn Leu Asp Leu Ile Arg Ser Thr Asn Lys Lys  
85 90 95

Gly Leu Ser Tyr Lys Leu Gly Val Asn Gln Phe Ala Asp Leu Thr Trp  
100 105 110

Gln Glu Phe Gln Arg Thr Lys Leu Gly Ala Ala Gln Asn Cys Ser Ala  
115 120 125

Thr Leu Lys Gly Ser His Lys Val Thr Glu Ala Ala Leu Pro Glu Thr  
130 135 140

Lys Asp Trp Arg Glu Asp Gly Ile Val Ser Pro Val Lys Asp Gln Gly  
145 150 155 160

Gly Cys Gly Ser Cys Trp Thr Phe Ser Thr Thr Gly Ala Leu Glu Ala  
165 170 175

Ala Tyr His Gln Ala Phe Ala Phe Gly Lys Gly Ile Ser Leu Ser Glu  
180 185 190

Gln Gln Leu Val Asp Cys Ala Gly Ala Phe Asn Asn Tyr Gly Cys Asn  
195 200 205

Gly Gly Leu Pro Ser Gln Ala Phe Glu Tyr Ile Lys Ser Asn Gly Gly  
210 215 220

Leu Asp Thr Glu Lys Ala Tyr Pro Tyr Thr Gly Lys Asp Glu Thr Cys  
225 230 235 240

Lys Phe Ser Ala Glu Asn Val Gly Val Gln Val Leu Asn Ser Val Ser  
245 250 255

Ile Thr Leu Gly Ala Glu Asp Glu Leu Lys His Ala Val Gly Leu Val  
260 265 270

Arg Pro Val Ser Ile Ala Phe Glu Val Ile His Ser Phe Arg Leu Tyr  
275 280 285

Lys Ser Gly Val Tyr Thr Asp Ser His Cys Gly Ser Thr Pro Met Asp  
290 295 300

Val Asn His Ala Val Leu Ala Val Gly Tyr Gly Val Glu Asp Gly Val  
305 310 315 320

Pro Tyr Trp Leu Ile Lys Asn Ser Trp Gly Ala Asp Trp Gly Asp Lys  
325 330 335

10087714.022800

## DMCI0099.ST25.txt

Gly Tyr Phe Lys Met Glu Met Gly Lys Asn Met Cys Gly Ile Ala Thr  
 340 345 350

Cys Ala Ser Tyr Pro Val Val Ala  
 355 360

<210> 21  
 <211> 362  
 <212> PRT  
 <213> Hordeum vulgare

<400> 21

Met Ala His Ala Arg Val Leu Leu Leu Ala Leu Ala Val Leu Ala Thr  
 1 5 10 15

Ala Ala Val Ala Val Ala Ser Ser Ser Ser Phe Ala Asp Ser Asn Pro  
 20 25 30

Ile Arg Pro Val Thr Asp Arg Ala Ala Ser Thr Leu Glu Ser Ala Val  
 35 40 45

Leu Gly Ala Leu Gly Arg Thr Arg His Ala Leu Arg Phe Ala Arg Phe  
 50 55 60

Ala Val Arg Tyr Gly Lys Ser Tyr Glu Ser Ala Ala Glu Val Arg Arg  
 65 70 75 80

Arg Phe Arg Ile Phe Ser Glu Ser Leu Glu Glu Val Arg Ser Thr Asn  
 85 90 95

Arg Lys Gly Leu Pro Tyr Arg Leu Gly Ile Asn Arg Phe Ser Asp Met  
 100 105 110

Ser Trp Glu Glu Phe Gln Ala Thr Arg Leu Gly Ala Ala Gln Thr Cys  
 115 120 125

Ser Ala Thr Lys Gly Asn His Leu Met Arg Asp Ala Ala Ala Leu Pro  
 130 135 140

Glu Thr Lys Asp Trp Arg Glu Asp Gly Ile Val Ser Pro Val Lys Asn  
 145 150 155 160

Gln Ala His Cys Gly Ser Cys Trp Thr Phe Ser Thr Thr Gly Ala Leu  
 165 170 175

Glu Ala Ala Tyr Thr Gln Ala Thr Gly Lys Asn Ile Ser Leu Ser Glu  
 180 185 190

Gln Gln Leu Val Asp Cys Ala Gly Gly Phe Asn Asn Phe Gly Cys Asn  
 Page 12

195

200

205

Gly Gly Leu Pro Ser Gln Ala Phe Glu Tyr Ile Lys Tyr Asn Gly Gly  
 210 215 220

Ile Asp Thr Glu Glu Ser Tyr Pro Tyr Lys Gly Val Asn Gly Val Cys  
 225 230 235 240

His Tyr Lys Ala Glu Asn Ala Ala Val Gln Val Leu Asp Ser Val Asn  
 245 250 255

Ile Thr Leu Asn Ala Glu Asp Glu Leu Lys Asn Ala Val Gly Leu Val  
 260 265 270

Arg Pro Val Ser Val Ala Ala Phe Gln Val Ile Asp Gly Phe Arg Gln  
 275 280 285

Tyr Lys Ser Gly Val Tyr Thr Ser Asp His Cys Gly Thr Thr Pro Asp  
 290 295 300

Asp Val Asn His Ala Val Leu Ala Val Gly Tyr Gly Val Glu Asn Gly  
 305 310 315 320

Val Pro Tyr Trp Leu Ile Lys Asn Ser Trp Gly Ala Asp Trp Gly Asp  
 325 330 335

Asn Gly Tyr Phe Lys Met Glu Met Gly Lys Asn Met Cys Ala Ile Ala  
 340 345 350

Thr Cys Ala Ser Tyr Pro Val Val Ala Ala  
 355 360

<210> 22  
 <211> 360  
 <212> PRT  
 <213> Nicotiana tobaccum

<400> 22

Met Ser Arg Phe Ser Leu Leu Leu Ala Leu Val Val Ala Gly Gly Leu  
 1 5 10 15

Phe Ala Ser Ala Leu Ala Gly Pro Ala Thr Phe Ala Asp Glu Asn Pro  
 20 25 30

Ile Arg Gln Val Val Ser Asp Gly Leu His Glu Leu Glu Asn Ala Ile  
 35 40 45

Leu Gln Val Val Gly Lys Thr Arg His Ala Leu Ser Phe Ala Arg Phe  
 50 55 60

## DMCI0099.ST25.txt

Ala His Arg Tyr Gly Lys Arg Tyr Glu Ser Val Glu Glu Ile Lys Gln  
65 70 75 80

Arg Phe Glu Val Phe Leu Asp Asn Leu Lys Met Ile Arg Ser His Asn  
85 90 95

Lys Lys Gly Leu Ser Tyr Lys Leu Gly Val Asn Glu Phe Thr Asp Leu  
100 105 110

Thr Trp Asp Glu Phe Arg Arg Asp Arg Leu Gly Ala Ala Gln Asn Cys  
115 120 125

Ser Ala Thr Thr Lys Gly Asn Leu Lys Val Thr Asn Val Val Leu Pro  
130 135 140

Glu Thr Lys Asp Trp Arg Glu Ala Gly Ile Val Ser Pro Val Lys Asn  
145 150 155 160

Gln Gly Lys Cys Gly Ser Cys Trp Thr Phe Ser Thr Thr Gly Ala Leu  
165 170 175

Glu Ala Ala Tyr Ser Gln Ala Phe Gly Lys Gly Ile Ser Leu Ser Glu  
180 185 190

Gln Gln Leu Val Asp Cys Ala Gly Ala Phe Asn Asn Phe Gly Cys Asn  
195 200 205

Gly Gly Leu Pro Ser Gln Ala Phe Glu Tyr Ile Lys Ser Asn Gly Gly  
210 215 220

Leu Asp Thr Glu Glu Ala Tyr Pro Tyr Thr Gly Lys Asn Gly Leu Cys  
225 230 235 240

Lys Phe Ser Ser Glu Asn Val Gly Val Lys Val Ile Asp Ser Val Asn  
245 250 255

Ile Thr Leu Gly Ala Glu Asp Glu Leu Lys Tyr Ala Val Ala Leu Val  
260 265 270

Arg Pro Val Ser Ile Ala Phe Glu Val Ile Lys Gly Phe Lys Gln Tyr  
275 280 285

Lys Ser Gly Val Tyr Thr Ser Thr Glu Cys Gly Asn Thr Pro Met Asp  
290 295 300

Val Asn His Ala Val Leu Ala Val Gly Tyr Gly Val Glu Asp Gly Val  
305 310 315 320

10087714-022802

Pro Tyr Trp Leu Ile Lys Asn Ser Trp Gly Ala Asp Trp Gly Asp Glu  
325 330 335

Gly Tyr Phe Lys Met Glu Met Gly Lys Asn Met Cys Gly Val Ala Thr  
340 345 350

Cys Ala Ser Tyr Pro Val Val Ala  
355 360

<210> 23  
<211> 360  
<212> PRT  
<213> Zea mays

<400> 23

Met Ala Pro Arg Arg Leu Leu Val Leu Ala<sup>c</sup> Val Val Ala Leu Ala Ala  
1 5 10 15

Thr Ala Ala Ala Ala Asn Ser Gly Phe Ala Asp Ser Asn Pro Ile Arg  
20 25 30

Pro Val Thr Asp Arg Ala Ala Ser Ala Leu Glu Ser Thr Val Phe Ala  
35 40 45

Ala Leu Gly Arg Thr Arg Asp Ala Leu Arg Phe Ala Arg Phe Ala Val  
50 55 60

Arg Tyr Gly Lys Ser Tyr Glu Ser Ala Ala Glu Val His Lys Arg Phe  
65 70 75 80

Arg Ile Phe Ser Glu Ser Leu Gln Leu Val Arg Ser Thr Asn Arg Lys  
85 90 95

Gly Leu Ser Tyr Arg Leu Gly Ile Asn Arg Phe Ala Asp Met Ser Trp  
100 105 110

Glu Glu Phe Arg Ala Thr Arg Leu Gly Ala Ala Gln Asn Cys Ser Ala  
115 120 125

Thr Leu Thr Gly Asn His Arg Met Arg Ala Ala Ala Val Ala Leu Pro  
130 135 140

Glu Thr Lys Asp Trp Arg Glu Asp Gly Ile Val Ser Pro Val Lys Asn  
145 150 155 160

Gln Gly His Cys Gly Ser Cys Trp Thr Phe Ser Thr Thr Gly Ala Leu  
165 170 175

DMCI0099.ST25.txt

Glu Ala Ala Tyr Thr Gln Ala Thr Gly Lys Pro Ile Ser Leu Ser Glu  
180 185 190

Gln Gln Leu Val Asp Cys Gly Leu Ala Phe Asn Asn Phe Gly Cys Asn  
195 200 205

Gly Gly Leu Pro Ser Gln Ala Phe Glu Tyr Ile Lys Tyr Asn Gly Gly  
210 215 220

Leu Asp Thr Glu Glu Ser Tyr Pro Tyr Gln Gly Val Asn Gly Ile Ser  
225 230 235 240

Lys Phe Lys Asn Glu Asn Val Gly Val Lys Val Leu Asp Ser Val Asn  
245 250 255

Ile Thr Leu Gly Ala Glu Asp Glu Leu Lys Asp Ala Val Gly Leu Val  
260 265 270

Arg Pro Val Ser Val Ala Phe Glu Val Ile Thr Gly Phe Arg Leu Tyr  
275 280 285

Lys Ser Gly Val Val Thr Ser Asp His Cys Gly Thr Thr Pro Met Asp  
290 295 300

Val Asn His Ala Val Leu Ala Val Gly Tyr Gly Val Glu Asp Gly Val  
305 310 315 320

Pro Tyr Trp Leu Ile Lys Asn Ser Trp Gly Ala Asp Trp Gly Asp Glu  
325 330 335

Gly Tyr Phe Lys Met Glu Met Gly Lys Asn Met Cys Gly Val Ala Thr  
340 345 350

Cys Ala Ser Tyr Pro Ile Val Ala  
355 360

<210> 24  
<211> 363  
<212> PRT  
<213> Zea mays

<400> 24

Met Ala His Arg Arg Ile Ile Leu Leu Leu Ala Val Ala Ala Val Ala  
1 5 10 15

Ala Thr Ser Ala Val Ala Ala Ala Ser Ser Gly Phe Asp Asp Ser Asn  
20 25 30



## DMCI0099.ST25.txt

Pro Ile Arg Pro Val Thr Asp Arg Ala Ala Ser Ala Leu Glu Ser Thr  
35 40 45

Val Phe Ala Ala Leu Gly Arg Thr Arg Asp Ala Leu Arg Phe Ala Arg  
50 55 60

Phe Ala Val Arg Tyr Gly Lys Ser Tyr Glu Ser Ala Ala Glu Val His  
65 70 75 80

Lys Arg Phe Arg Ile Phe Ser Glu Ser Leu Gln Leu Val Arg Ser Thr  
85 90 95

Asn Arg Lys Gly Leu Ser Tyr Arg Leu Gly Tyr Asn Arg Phe Ala Asp  
100 105 110

Met Ser Trp Glu Glu Phe Arg Ala Thr Arg Leu Gly Ala Ala Gln Asn  
115 120 125

Cys Ser Ala Thr Leu Thr Gly Asn His Arg Met Arg Ala Ala Ala Val  
130 135 140

Ala Leu Pro Glu Thr Lys Asp Trp Arg Glu Asp Gly Ile Val Ser Pro  
145 150 155 160

Val Lys Asn Gln Gly His Cys Gly Ser Cys Trp Thr Phe Ser Thr Thr  
165 170 175

Gly Ala Leu Glu Ala Ala Tyr Thr Gln Ala Thr Gly Lys Pro Ile Ser  
180 185 190

Leu Ser Glu Gln Gln Leu Val Asp Cys Gly Phe Ala Phe Asn Asn Phe  
195 200 205

Gly Cys Asn Gly Gly Leu Pro Ser Gln Ala Phe Glu Tyr Ile Lys Tyr  
210 215 220

Asn Gly Gly Leu Asp Thr Glu Glu Ser Tyr Pro Tyr Gln Gly Val Asn  
225 230 235 240

Gly Ile Cys Lys Phe Lys Asn Glu Asn Val Gly Val Lys Val Leu Asp  
245 250 255

Ser Val Asn Ile Thr Leu Gly Ala Glu Asp Glu Leu Lys Asp Ala Val  
260 265 270

Gly Leu Val Arg Pro Val Ser Val Ala Phe Glu Val Ile Thr Gly Phe  
275 280 285

## DMCI0099.ST25.txt

Arg Leu Tyr Lys Ser Gly Val Tyr Thr Ser Asp His Cys Gly Thr Thr  
290 295 300

Pro Met Asp Val Asn His Ala Val Leu Ala Val Gly Tyr Gly Val Glu  
305 310 315 320

Asp Gly Val Pro Tyr Trp Leu Ile Lys Asn Ser Trp Gly Ala Asp Trp  
325 330 335

Gly Asp Glu Gly Tyr Phe Lys Met Glu Met Gly Lys Asn Met Cys Gly  
340 345 350

Val Ala Thr Cys Ala Ser Tyr Pro Ile Val Ala  
355 360

<210> 25

<211> 362

<212> PRT

<213> Oryza sativa

<400> 25

Met Ala His Arg Arg Ile Ile Leu Leu Leu Ala Val Ala Ala Val Ala  
1 5 10 15

Ala Thr Ser Ala Val Ala Ala Ala Ser Ser Gly Phe Asp Asp Ser Asn  
20 25 30

Pro Ile Arg Ser Val Thr Asp His Ala Ala Ser Ala Leu Glu Ser Thr  
35 40 45

Val Ile Ala Ala Leu Gly Arg Thr Arg Gly Ala Leu Arg Phe Ala Arg  
50 55 60

Phe Ala Val Arg Gly His Lys Arg Tyr Gly Asp Ala Ala Glu Val Gln  
65 70 75 80

Arg Arg Phe Arg Ile Phe Ser Glu Ser Leu Glu Leu Val Arg Ser Thr  
85 90 95

Asn Arg Arg Gly Leu Pro Tyr Arg Leu Gly Ile Asn Arg Phe Ala Asp  
100 105 110

Met Ser Trp Glu Glu Phe Gln Ala Ser Arg Leu Gly Ala Ala Gln Asn  
115 120 125

Cys Ser Ala Thr Leu Ala Gly Asn His Arg Met Arg Asp Ala Pro Ala  
130 135 140

Leu Pro Glu Thr Lys Asp Trp Arg Glu Asp Gly Ile Val Ser Pro Val  
Page 18

10087714-022802

145                      150                      155                      160  
 Lys Asp Gln Gly His Cys Gly Ser Cys Trp Pro Phe Ser Thr Thr Gly  
                                  165                                   170                                   175  
 Ser Leu Glu Ala Arg Tyr Thr Gln Ala Thr Gly Pro Pro Val Ser Leu  
                                  180                                   185                                   190  
 Ser Glu Gln Gln Leu Ala Asp Cys Ala Thr Arg Tyr Asn Asn Phe Gly  
                                  195                                   200                                   205  
 Cys Ser Gly Gly Leu Pro Ser Gln Ala Phe Glu Tyr Ile Lys Tyr Asn  
                                  210                                   215                                   220  
 Gly Gly Leu Asp Thr Glu Glu Ala Tyr Pro Tyr Thr Gly Val Asn Gly  
                                  225                                   230                                   235                                   240  
 Ile Cys His Tyr Lys Pro Glu Asn Ala Gly His Lys Val Leu Asp Ser  
                                  245                                   250                                   255  
 Val Asn Ile Thr Leu Val Ala Glu Asp Glu Leu Lys Asn Ala Val Gly  
                                  260                                   265                                   270  
 Leu Val Arg Pro Val Ser Val Ala Phe Gln Val Ile Asn Gly Phe Arg  
                                  275                                   280                                   285  
 Met Tyr Lys Ser Gly Val Tyr Thr Ser Asp His Cys Gly Thr Ser Pro  
                                  290                                   295                                   300  
 Met Asp Val Asn His Ala Val Leu Ala Val Gly Tyr Gly Val Glu Asn  
                                  305                                   310                                   315                                   320  
 Gly Val Pro Tyr Trp Leu Ile Lys Asn Ser Trp Gly Ala Asp Trp Gly  
                                  325                                   330                                   335  
 Asp Asn Gly Tyr Phe Thr Met Glu Met Gly Lys Asn Met Cys Gly Ile  
                                  340                                   345                                   350  
 Ala Thr Cys Ala Ser Tyr Pro Ile Val Ala  
                                  355                                   360